

Serial Number: 09/292,202

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:
-
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
-
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
-
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
-
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:
-
- ☐ Deleted extra, invalid, headings used by an applicant, specifically:
-
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically:
-
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:
-
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 20 - corrected amino acid numbering
-

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JUN 9 2000
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*Examiner: ~~The above~~ corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING DATE: 05/28/2000
 PATENT APPLICATION: US/09/242,202 TIME: 15:24:43

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\05262000\I242202.raw

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C--> 5 (1) GENERAL INFORMATION:
C--> 7   (i) APPLICANT: Nelson, Edward L.
      8           Nelson, Peter J.
C--> 10  (ii) TITLE OF INVENTION: NOVEL VECTOR FOR
      11           POLYNUCLEOTIDE VACCINES
C--> 13  (iii) NUMBER OF SEQUENCES: 29
C--> 15  (iv) CORRESPONDENCE ADDRESS:
C--> 16      (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
C--> 17      (B) STREET: 345 PARK AVENUE
C--> 18      (C) CITY: NEW YORK
C--> 19      (D) STATE: NEW YORK
C--> 20      (E) COUNTRY: USA
C--> 21      (F) ZIP: 10154
C--> 23  (v) COMPUTER READABLE FORM:
C--> 24      (A) MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
C--> 25      (B) COMPUTER: IBM PC COMPATIBLE
C--> 26      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
C--> 27      (D) SOFTWARE: MS WORD 97
C--> 30  (vi) CURRENT APPLICATION DATA:
C--> 31      (A) APPLICATION NUMBER: US/09/242,202
C--> 32      (B) FILING DATE: 01-Nov-1999
C--> 34  (vii) PRIOR APPLICATION DATA:
C--> 35      (A) APPLICATION NUMBER: US60/023931
C--> 36      (B) FILING DATE: 14-AUG-1996
C--> 38  (viii) ATTORNEY/AGENT INFORMATION:
C--> 39      (A) NAME: KATHRYN M. BROWN
C--> 40      (B) REGISTRATION NUMBER: 34556
C--> 41      (C) REFERENCE/DOCKET NUMBER: 2026-4236US1
C--> 43  (ix) TELECOMMUNICATION INFORMATION:
C--> 44      (A) TELEPHONE: (212) 758-4800
C--> 45      (B) TELEFAX: (212) 751-6849
C--> 46      (C) TELEX: 421792
C--> 48 (2) INFORMATION FOR SEQ ID NO: 1:
C--> 50   (i) SEQUENCE CHARACTERISTICS:
C--> 51      (A) LENGTH: 453 base pairs
C--> 52      (B) TYPE: nucleic acid
C--> 53      (C) STRANDEDNESS: single
C--> 54      (D) TOPOLOGY: unknown
C--> 56   (ii) MOLECULE TYPE: cDNA
C--> 62   (iii) HYPOTHETICAL: No
C--> 64   (iv) ANTI-SENSE: No
C--> 66   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
      68 GGC CGC GTT G CTGGCGTTT TCCATAGGCT CCGCCCCCCT      40
      69 GACGAGCATC ACAAAAATCG ACGCTCAAGT CAGAGGTGGC      80
      70 GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC     120
      71 TGGAGCTCC CTCGTGCGCT CTCCTGTTC GACCCTGCCG      160
      72 CTTACCGGAT ACCTCTCCGC CTTTCTCCCT TCGGGAAGCG      200

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73 TGGCGCTTTC TCAATGCTCA CGCTGTAGGT ATCTCAGTTC      240
74 GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA      280
75 CCCCCCGTTC AGCCCGACCG CTGCGCCTTA TCCGGTAACT      320
76 ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC      360
77 ACTGGCAGCA GCCACTGGTA ACAGGATTAG CAGAGCGAGG      400
78 TATGTAGGCG GTGCTACAGA GTTCTTGAAG TGGTGGCCTA      440
79 ACTACGGCTA CAC                                     453

C--> 82 (2) INFORMATION FOR SEQ ID NO: 2:
C--> 84 (i) SEQUENCE CHARACTERISTICS:
C--> 85 (A) LENGTH: 453 base pairs
C--> 86 (B) TYPE: nucleic acid
C--> 88 (C) STRANDEDNESS: single
C--> 89 (D) TOPOLOGY: unknown
C--> 91 (ii) MOLECULE TYPE: cDNA
C--> 93 (iii) HYPOTHETICAL: No
C--> 95 (iv) ANTI-SENSE: No
C--> 97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
99 GTGTAGCCGT AGTTAGGCCA CCACTTCAAG AACTCTGTAG      40
100 CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTTACCAGT      80
101 GGCTGCTGCC AGTGGCGATA AGTCGTGTCT TACCGGGTTG     120
102 GACTCAAGAC GATAGTTACC GGATAAGGCG CAGCGGTCGG     160
103 GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG     200
104 AACGACCTAC ACCGAAC TGA GATACCTACA CCGTGAGCAT     240
105 TGAGAAAGCG CCACGCTTCC CGAAGGGAGA AAGGCGGACA     280
106 GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC     320
107 GAGGGAGCTT CCAGGGGGAA ACGCCTGGTA TCTTTATAGT     360
108 CCTGTGCGGT TTCGCCACCT CTGACTTGAG CGTCGATTTT     400
109 TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC     440
110 CAGCAACGCG GCC                                     453

C--> 113 (2) INFORMATION FOR SEQ ID NO: 3:
C--> 115 (i) SEQUENCE CHARACTERISTICS:
C--> 116 (A) LENGTH: 209 base pairs
C--> 122 (B) TYPE: nucleic acid
C--> 123 (C) STRANDEDNESS: single
C--> 124 (D) TOPOLOGY: unknown
C--> 126 (ii) MOLECULE TYPE: cDNA
C--> 128 (iii) HYPOTHETICAL: No
C--> 130 (iv) ANTI-SENSE: No
C--> 132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
134 GAATTCTTTC GGACTTTTGA AAGTGATGGT GGTGGCCGAA      40
135 GGATTCTGAAC CTTCGAAGTC GATGACGGCA GATTTAGAGT      80
136 CTGCTCCCTT TGGCCGCTCG GGAACCCAC CACGGGTAAT     120
137 GCTTTTACTG GCCTGCTCCC TTATCGGGAA GCGGGGCGCA     160
138 TCATATCAAA TGACGCGCCG CTGTAAAGTG TTACGTGAG      200
139 AAAGAATTC                                     209

C--> 142 (2) INFORMATION FOR SEQ ID NO: 4:
C--> 144 (i) SEQUENCE CHARACTERISTICS:
C--> 145 (A) LENGTH: 209 base pairs
C--> 147 (B) TYPE: nucleic acid

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C--> 148      (C) STRANDEDNESS: single
C--> 149      (D) TOPOLOGY: unknown
C--> 151      (ii) MOLECULE TYPE: cDNA
C--> 153      (iii) HYPOTHETICAL: No
C--> 155      (iv) ANTI-SENSE: No
C--> 157      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
159 GAATTCCTTC TCAACGTAAC ACTTTACAGC GGCGCGTCAT      40
160 TTGATATGAT GCGCCCCGCT TCCCGATAAG GGAGCAGGCC      80
161 AGTAAAGCA TTACCCGTGG TGGGGTTCCC GAGCGGCCAA      120
162 AGGGAGCAGA CTCTAAATCT GCCGTCATCG ACTTCGAAGG      160
163 TTCGAATCCT TCCCCACCA CCATCACTTT CAAAAGTCCG      200
164 AAAGAATTC      209

C--> 167 (2) INFORMATION FOR SEQ ID NO: 5:
C--> 169      (i) SEQUENCE CHARACTERISTICS:
C--> 170          (A) LENGTH: 6 base pairs
C--> 171          (B) TYPE: nucleic acid
C--> 172          (C) STRANDEDNESS: single
C--> 173          (D) TOPOLOGY: unknown
C--> 175      (ii) MOLECULE TYPE: cDNA
C--> 182      (iii) HYPOTHETICAL: No
C--> 184      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
187 AATAAA      6

C--> 190 (2) INFORMATION FOR SEQ ID NO: 6:
C--> 192      (i) SEQUENCE CHARACTERISTICS:
C--> 193          (A) LENGTH: 6 base pairs
C--> 194          (B) TYPE: nucleic acid
C--> 195          (C) STRANDEDNESS: single
C--> 196          (D) TOPOLOGY: unknown
C--> 198      (ii) MOLECULE TYPE: cDNA
C--> 200      (iii) HYPOTHETICAL: No
C--> 202      (iv) ANTI-SENSE: No
C--> 204      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
208 ATTAAA      6

C--> 211 (2) INFORMATION FOR SEQ ID NO: 7:
C--> 213      (i) SEQUENCE CHARACTERISTICS:
C--> 214          (A) LENGTH: 6 base pairs
C--> 215          (B) TYPE: nucleic acid
C--> 216          (C) STRANDEDNESS: single
C--> 217          (D) TOPOLOGY: unknown
C--> 219      (ii) MOLECULE TYPE: cDNA
C--> 221      (iii) HYPOTHETICAL: No
C--> 223      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
226 AGTAAA      6

C--> 229 (2) INFORMATION FOR SEQ ID NO: 8:
C--> 231      (i) SEQUENCE CHARACTERISTICS:
C--> 232          (A) LENGTH: 6 base pairs
C--> 233          (B) TYPE: nucleic acid
C--> 234          (C) STRANDEDNESS: single
C--> 235          (D) TOPOLOGY: unknown

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 PATENT APPLICATION: US/09/242,202 TIME: 15:24:43

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 Output Set: N:\CRF3\05262000\I242202.raw

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C--> 237      (ii) MOLECULE TYPE: cDNA
C--> 244      (iii) HYPOTHETICAL: No
C--> 246      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
    249 AAGAAC                                     6
C--> 252 (2) INFORMATION FOR SEQ ID NO: 9:
C--> 254      (i) SEQUENCE CHARACTERISTICS:
C--> 255          (A) LENGTH: 6 base pairs
C--> 256          (B) TYPE: nucleic acid
C--> 257          (C) STRANDEDNESS: single
C--> 258          (D) TOPOLOGY: unknown
C--> 260      (ii) MOLECULE TYPE: cDNA
C--> 262      (iii) HYPOTHETICAL: No
C--> 264      (iv) ANTI-SENSE: No
C--> 266      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
    269 AATACA                                     6
C--> 272 (2) INFORMATION FOR SEQ ID NO: 10:
C--> 274      (i) SEQUENCE CHARACTERISTICS:
C--> 275          (A) LENGTH: 227 base pairs
C--> 276          (B) TYPE: nucleic acid
C--> 277          (C) STRANDEDNESS: single
C--> 278          (D) TOPOLOGY: unknown
C--> 280      (ii) MOLECULE TYPE: cDNA
C--> 282      (iii) HYPOTHETICAL: No
C--> 284      (iv) ANTI-SENSE: No
C--> 286      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
    289 GCCTTAAGGG CCATATGGTG AGTGGATCCC TTGACCCAG      40
    290 GCGGGGATGG GGAGACCTGT AGTCAGAGCC CCCGGGCAGC      80
    291 ACAGGCCAAT GCCCGTCCTT CCCCTGCAGG ATGAGTAGTG     120
    292 AGTGCCTCTC CTGGCCCTGG AAGTTGCCAC TCCAGTGCCC     160
    293 ACCAGCCTTG TCCTAATAAA ATTAAGTTGC ATCATTTTGT     200
    294 CTGACTAGGT GTCCTCTATA ATATTAT      227
C--> 297 (2) INFORMATION FOR SEQ ID NO: 11:
C--> 299      (i) SEQUENCE CHARACTERISTICS:
C--> 300          (A) LENGTH: 227 base pairs
C--> 301          (B) TYPE: nucleic acid
C--> 307          (C) STRANDEDNESS: single
C--> 308          (D) TOPOLOGY: unknown
C--> 310      (ii) MOLECULE TYPE: cDNA
C--> 312      (iii) HYPOTHETICAL: No
C--> 314      (iv) ANTI-SENSE: No
C--> 316      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
    319 ATAATATTAT AGAGGACACC TAGTCAGAAC AAATGATGCA      40
    320 ACTTAATTTT ATTAGGACAA GGCTGGTGGG CACTGGAGTG      80
    321 GCAACTTCCA GGGCCAGGAG AGGCACTCAC TACTCATCCT     120
    322 GCAGGGGAAG GACGGGCATT GGCTGTGCT GCCCGGGGGC     160
    323 TCTGACTACA GGTCTCCCCC ATCCCCGCCT GGGGTCAAGG     200
    324 CATCCACTCA CCATATGGCC CTTAAGG      227
C--> 327 (2) INFORMATION FOR SEQ ID NO: 12:
C--> 329      (i) SEQUENCE CHARACTERISTICS:

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C--> 330      (A) LENGTH: 252 base pairs
C--> 331      (B) TYPE: nucleic acid
C--> 332      (C) STRANDEDNESS: single
C--> 333      (D) TOPOLOGY: unknown
C--> 335      (ii) MOLECULE TYPE: cDNA
C--> 337      (iii) HYPOTHETICAL: No
C--> 339      (iv) ANTI-SENSE: No
C--> 341      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
    344 CCTCGGTACC TGCCATGGCG CGGATCTTT ATCACTGATA      40
    345 AGTTGGTGGA CATATTATGT TTATCAGTGA TAAAGTGTCA      80
    346 AGCATGACAA AGTTGCAGCC GAATACAGTG ATCCGTGCCG     120
    347 GCCCTGGACT GTTGAACGAG GTCGGCGTAG ACGGTCTGAC     160
    348 GACACGCAA CTGGCGGAAC GGTGGGGGT GCAGCAGCCG     200
    349 GCGCTTTACT GGCACCTTAG GAACAAGCGG GCGCCTTAAG     240
    350 GGCCATATGC CG                                  252

C--> 353 (2) INFORMATION FOR SEQ ID NO: 13:
C--> 355      (i) SEQUENCE CHARACTERISTICS:
C--> 356      (A) LENGTH: 35 base pairs
C--> 357      (B) TYPE: nucleic acid
C--> 358      (C) STRANDEDNESS: single
C--> 359      (D) TOPOLOGY: unknown
C--> 365      (ii) MOLECULE TYPE: cDNA
C--> 367      (iii) HYPOTHETICAL: No
C--> 369      (iv) ANTI-SENSE: No
C--> 371      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
    374 CCTCGGTACC TGCCACCATG GCGCGGATTC TTTAT          35

C--> 377 (2) INFORMATION FOR SEQ ID NO: 14:
C--> 379      (i) SEQUENCE CHARACTERISTICS:
C--> 380      (A) LENGTH: 38 base pairs
C--> 381      (B) TYPE: nucleic acid
C--> 382      (C) STRANDEDNESS: single
C--> 383      (D) TOPOLOGY: unknown
C--> 385      (ii) MOLECULE TYPE: cDNA
C--> 387      (iii) HYPOTHETICAL: No
C--> 389      (iv) ANTI-SENSE: No
C--> 391      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
    394 CGGCATATGG CCTTAAGCG CCCGCTTGT CCTGAAGT          38

C--> 397 (2) INFORMATION FOR SEQ ID NO: 15:
C--> 399      (i) SEQUENCE CHARACTERISTICS:
C--> 400      (A) LENGTH: 228 base pairs
C--> 401      (B) TYPE: nucleic acid
C--> 402      (C) STRANDEDNESS: single
C--> 403      (D) TOPOLOGY: unknown
C--> 405      (ii) MOLECULE TYPE: cDNA
C--> 407      (iii) HYPOTHETICAL: No
C--> 409      (iv) ANTI-SENSE: No
C--> 411      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
    413 GCCTTAAGGG CCATATGGTG AGTGGATGCC TTGACCCAG      40
    414 GCGGGGATGG GGGAGACCTG TAGTCAGAGC CCCCggGCAG      80
  
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/242,202

DATE: 05/28/2000

TIME: 15:24:44

Input Set : A:\Pto.amc

Output Set: N:\CRF3\05262000\I242202.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:7 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:10 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:13 M:220 C: Keyword misspelled or invalid format, [(iii) NUMBER OF SEQUENCES:]
L:15 M:220 C: Keyword misspelled or invalid format, [(iv) CORRESPONDENCE ADDRESS:]
L:16 M:220 C: Keyword misspelled or invalid format, [(A) ADDRESSEE:]
L:17 M:220 C: Keyword misspelled or invalid format, [(B) STREET:]
L:18 M:220 C: Keyword misspelled or invalid format, [(C) CITY:]
L:19 M:220 C: Keyword misspelled or invalid format, [(D) STATE:]
L:20 M:220 C: Keyword misspelled or invalid format, [(E) COUNTRY:]
L:21 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:23 M:220 C: Keyword misspelled or invalid format, [(v) COMPUTER READABLE FORM:]
L:24 M:220 C: Keyword misspelled or invalid format, [(A) MEDIUM TYPE:]
L:25 M:220 C: Keyword misspelled or invalid format, [(B) COMPUTER:]
L:26 M:220 C: Keyword misspelled or invalid format, [(C) OPERATING SYSTEM:]
L:27 M:220 C: Keyword misspelled or invalid format, [(D) SOFTWARE:]
L:30 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
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L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:38 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:39 M:220 C: Keyword misspelled or invalid format, [(A) NAME:]
L:40 M:220 C: Keyword misspelled or invalid format, [(B) REGISTRATION NUMBER:]
L:41 M:220 C: Keyword misspelled or invalid format, [(C) REFERENCE/DOCKET NUMBER:]
L:43 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:44 M:220 C: Keyword misspelled or invalid format, [(A) TELEPHONE:]
L:45 M:220 C: Keyword misspelled or invalid format, [(B) TELEFAX:]
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L:48 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:50 M:220 C: Keyword misspelled or invalid format, [(i) SEQUENCE CHARACTERISTICS:]
L:51 M:220 C: Keyword misspelled or invalid format, [(A) LENGTH:]
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L:64 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:66 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
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L:89 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:91 M:220 C: Keyword misspelled or invalid format, [(ii) MOLECULE TYPE:]
L:93 M:220 C: Keyword misspelled or invalid format, [(iii) HYPOTHETICAL:]

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L:95 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:97 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:797 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23, Value=
[oligonucleotide]
L:817 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24, Value=
[oligonucleotide]